

1656

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/373,984

DATE: 01/24/2001

TIME: 13:39:03

Input Set : A:\23879002.txt

Output Set: N:\CRF3\01242001\I373984.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: SU, Xing
 4 ANDERSON, Rolfe
 6 <120> TITLE OF INVENTION: SINGLE-PHASE AMPLIFICATION OF NUCLEIC ACIDS
 8 <130> FILE REFERENCE: 23879.0002
 10 <140> CURRENT APPLICATION NUMBER: 09/373,984
 11 <141> CURRENT FILING DATE: 1999-08-16
 13 <150> PRIOR APPLICATION NUMBER: 60/146,142
 14 <151> PRIOR FILING DATE: 1999-07-30
 16 <160> NUMBER OF SEQ ID NOS: 1
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 59
 22 <212> TYPE: DNA
 23 <213> ORGANISM: unidentified
 25 <400> SEQUENCE: 1
 26 ggccagtgaatgtaatacg actcactata gggaggcgggt tttttttttt tttttttttt 59

*invalid - per 1.823 of new Sequence Rules, the
 only valid <213> responses are: Unknown,
 Artificial Sequence, or scientific name (Genus/species)*

↓
 (see circled portion of
 item 12 on Error
 Summary Sheet)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/373,984

DATE: 01/24/2001

TIME: 13:39:04

Input Set : A:\23879002.txt

Output Set: N:\CRF3\01242001\I373984.raw

RECEIVED
FEB 05 2001
TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/373,984

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | | | |
|----|------|----------------------------------|--|--|
| 1 | ____ | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". | <div style="font-size: 2em; font-weight: bold;">RECEIVED</div> <div style="font-size: 1.2em; font-weight: bold;">FEB 05 2001</div> <div style="font-size: 0.8em; font-weight: bold;">TECH CENTER 1600/2900</div> |
| 2 | ____ | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 3 | ____ | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. | |
| 4 | ____ | Misaligned Amino Acid Numbering | The numbering of each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. | |
| 5 | ____ | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. | |
| 6 | ____ | Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. | |
| 7 | ____ | PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 8 | ____ | Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). | |
| 9 | ____ | Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 | |
| 10 | ____ | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 11 | ____ | Use of <213>Organism (NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. | |
| 12 | ____ | Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) | |
| 13 | ____ | PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. | |